10. (New) An isolated cDNA consisting of the nucleotide sequence of Sequence ID No. 19.

REMARKS

The claims have been amended to better recite the patentable nature of the present invention. No new matter has been added.

Claim 11 (sic, claim 1?) is objected to for reciting an improper Markush group. In response, claim 1 (and claims 3 and 4) are amended to delete the nonelected subject matter. Accordingly, this objection is met.

Claims 1-6 stand objected to for use of non-idiomatic language. Although the language recited is not improper per se, it has nevertheless been corrected in conformity with the Examiner's kind suggestions in order to reduce the issues. Accordingly, this objection is met as well.

Claim 6 is objected to under 37 C.F.R. §1.75(c) and claims 5 and 6 rejected under 35 U.S.C. §112, second paragraph, as indefinite, for improper dependency. In response, the dependency of claims 5 and 6 has been corrected.

Claims 1 and 2 stand rejected under 35 U.S.C. §101 as directed to non statutory subject matter. In response, these claims have also been amended in conformity with the Examiner's suggestions. Accordingly, this rejection is overcome.

Claims 1-6 are rejected under 35 U.S.C. §101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

In this regard, the Examiner necessarily contends (i) the activity of the present invention is not credible since (ii) those of ordinary skill recognize protein activity cannot be predicted from known homologous sequences.[1/] According to the Examiner, implicitly at least, the pending claims do not satisfy the utility requirement of 35 USC 101 because, given the state of the art, structure-function analysis is unpredictable. This basis of rejection is, respectfully submitted, without foundation either in law or in fact.

As the Examiner is aware, HPO2000 encodes a protein obtained from human stomach cancer cDNA library that, when expressed, provides a transmembrane fraction containing a protein of the expected weight of the open reading frame. Applicants believe the protein is sufficiently similar to rat organic cation transporter (67.5% homology at the N-terminal 169 amino acid portion) that it evidences similar drug excretion-associated activity.

The Examiner's point concerning the unpredictability of protein activity from known homologous sequences is <u>not</u> well-taken by those of ordinary skill. See, e.g., Principles of Protein Structure, Cantor, ed. (1978) 167 wherein it is explicitly taught that

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1/ Regarding the Examiner's technical analyses of the unpredictable activity resulting from amino acid changes, such is simply <u>not</u> the current position of either those of ordinary skill, or the Patent and Trademark Office. That is, while changes do occur (and some are drastic), similarity is, nevertheless, now reasonably expected, as discussed below.

> "[h]omologous proteins result from speciation or differentiation. Comparisons between homologous proteins have yielded general rules for protein structures (citing Schulz, Angew. Chem. Int. Edit., Vol. 16 (1977) 23-33). . . . In this context it is often useful to distinguish between protein speciation and protein differentiation (citing Molecular evolution and Polymorphism, Kimura ed. (1977) National Institute of Genetics, Mishima, Japan). Speciation is the evolution of homologous proteins possessing a common function in different organisms."

This knowledge is summarized in the art as evidencing that establishing homology between the unknown and reference proteins permits the skilled artisan to assume the unknown unexpressed protein and the known reference protein have the same function (emphasis added). Functional Genomics, Science, Vol. 278, No. 601 (1997).

This is not an aberrant position; similarly, the American Society of Human Genetics ("ASHG") similarly acknowledges "sequence homology is a useful predictor of gene function." Letter from Ronald Worton, Ph.D., President, ASHG, to the Honorable Q. Todd Dickinson, Assistant Secretary of Commerce and Commissioner of Patents and Trademarks, Unites States Patent and Trademark Office at 2 (Mar. 22, 2000) (on file with the USPTO).

Additionally, the USPTO too recognizes the state of this art in Example 10 of the Utility Training Materials: DNA fragments encoding a Full Open Reading Frame (ORF). In that example, the Examiner is directed not to reject the claims merely because the applicant's asserted utility is premised on the "overall level of sequence similarity between SEQ ID NO:3 [the unknown sequence] and the consensus sequence of the known DNA ligases that are presented in the specification." Indeed, Example 10 acknowledges

that "homology between the known and unknown protein is sufficient to ascribe the known protein's function to the unknown; thus the claim possesses credible, substantial, and specific utility."[2/] (emphasis added.) Id. at 54.

Moreover, the Federal Circuit acknowledges as well utility is well-established if it is apparent to one skilled in the art[3/] ("genus claims to nucleic acids based on their hybridization properties, . . . [if the subject matter of the claims will] hybridize under highly stringent conditions to known sequences because such conditions dictate that all species within the genus will be structurally similar.") See Enzo Biochem v. Gen-Probe, Appeal No. 01-1230 slip op. granting reh'g at 15 (Fed. Cir. July 15, 2002).

Applicants wish to point out that, at the very least, the resemblance of the present invention to specific proteins of known activity makes it clear the present invention can be further utilized as research tools for better characterizing those prior art compounds. That asserted utility, e.g., to better characterize prior art organic cation transporters, is specific; specific utility does not exclude even generalized research tools like probes, when the target being probed for is already known. See the Revised Interim Utility Guidelines Training Materials at 50-53. See also the Federal Circuit Bar Journal, Vol. 11, No. 4 (2002) 918 wherein full-length homology-based sequences are found to have specific

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2/ In fact, the guidelines make clear there is no minimum percentage required and directs the Examining corp not to focus on numbers.

3/ Should the Examiner maintains Applicants' statements at specification pages 41-43 are vague, they will promptly file a Declaration under Rule 132 explicitly stating "SEQ ID NO:1 has sufficient homology with known organic cation transporter that those of ordinary skill expect it to exhibit such activity", if such will be helpful to the Examiner. Alternatively, the Examiner can take this representation as being made by authorization. Clarification in this regard is respectfully requested.

credible utility if the homologous prior art sequence has a known function, since their use as research tools is necessarily specific to the homologous prior art sequence.

Accordingly, respectfully submitted, the rejection under 35 U.S.C. § 101 is overcome and withdrawal thereof is earnestly solicited.

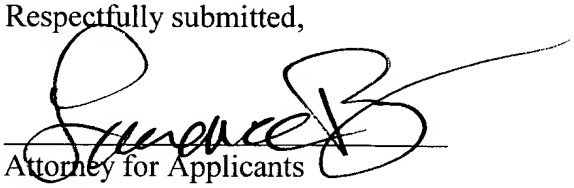
Claims 1-6 are also rejected under 35 U.S.C. §112 first paragraph. In support of this rejection, the Examiner states that because the invention is not supported by a substantial asserted utility, one of ordinary skill would not know how to use it. However, as seen explained above, the present invention is supported by a specific and substantial utility.

In view of the above amendments and remarks, Applicants submit that all of the Examiner's concerns are now overcome and the claims are now in allowable condition. Accordingly, reconsideration and allowance of this application is earnestly solicited.

Claims 1-3 and 5-10 remain presented for continued prosecution.

Applicants' undersigned attorney may be reached in our New York office by telephone at (212) 218-2100. All correspondence should continue to be directed to our below listed address.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE TO CLAIMS

1. (Amended) An isolated protein comprising [any of] the amino acid sequence[s represented by] of Sequence ID No[s]. 1 [to 9].

2. (Amended) An isolated DNA encoding [for any of] the protein[s as claimed in] of Claim 1.

3. (Amended) A cDNA comprising any of the [base] nucleotide sequence[s represented by] of Sequence ID Nos. 10 [to 18] or 19.

4. Cancelled.

5. (Amended) An express vector capable of expressing the DNA as claimed in any one of Claims 2 [to Claim 4], 3 or 8-10 by in vitro translation or transformation in eucaryotic cells.

6. (Amended) A transform[ation]ed eucaryotic cell harboring the expression vector of claim 5 and being capable of expressing [the DNA as claimed in any of Claim 2 to Claim 4 and producing] the protein [as claimed in Claim 1] of Sequence ID NO.1.